

A POPULATION BASED TWIN STUDY
EXAMINING THE RELATIONSHIP BETWEEN
SUBJECTIVE WELL-BEING AND MAJOR
DEPRESSION

BY

KNUT OSVALD HEIE ERTZEID

MASTER THESIS IN PSYCHOLOGY

INSTITUTE OF PSYCHOLOGY

UNIVERSITY OF OSLO

MAY 2010

ACKNOWLEDGMENTS

I would like to thank my supervisors Ragnhild Bang Nes and Nikolai Olavi Czajkowski. Both of them used a great deal of their valuable time (far more than what was requested of them) to educate and support me. This project was a result of my desire to write a thesis concerning the positive aspects of mental health. The possibility to look at both sides of the mental health spectrum evolved gradually through discussions with Ragnhild and Nikolai. I would like to thank the Norwegian Institute of Public Health, Division of Mental Health, for allowing me to use their data, and thanks to all the twins who have participated. Thanks to Espen Røysamb for his insightful contributions and for helping me find supervisors at the Norwegian Institute of Public Health. Last but not least I would like to thank my wife and family for their support.

ABSTRACT

Are happiness and depression related or completely distinct constructs? Using data from the Norwegian Institute of Public Health Twin Panel, we investigated the common and specific genetic and environmental contributions to subjective well-being (SWB) and liability to lifetime major depression. The results show that a substantial portion of both genetic and non-shared environmental variance is shared between major depressive disorder and SWB. These findings indicate that intervention and treatment aiming to increase SWB may decrease the risk of major depression. Results also indicate that morbidity and vitality may not be entirely distinct constructs at least from a genetic point of view.

TABLE OF CONTENTS

INTRODUCTION.....	1
Subjective Well-Being.....	1
<i>The etiology of SWB.....</i>	<i>3</i>
Major Depression	5
<i>The etiology of Major depression</i>	<i>6</i>
Behavior Genetics.....	9
<i>A Brief History</i>	<i>9</i>
<i>Important concepts in behavior genetics</i>	<i>10</i>
<i>Genetic Effects</i>	<i>10</i>
<i>Environmental Effects.....</i>	<i>11</i>
<i>Genotype- Environment Interplay.....</i>	<i>12</i>
<i>Twin Method Assumptions - Assortative Mating</i>	<i>14</i>
<i>Twin Method Assumptions - The Equal Environment Assumption (EEA).....</i>	<i>14</i>
<i>Genetic Epidemiology and Psychiatric Genetics.....</i>	<i>15</i>
METHODS	16
Sample	16
Measures	17
Statistical analysis.....	18
Structural Equation Modeling	20
Variance Component	20
Path Analysis	22
RESULTS.....	24
DISCUSSION	30
<i>Univariate analysis</i>	<i>31</i>

<i>Multivariate analysis</i>	<i>31</i>
<i>Correlation between Major Depression and Subjective Well-Being.....</i>	<i>32</i>
STUDY LIMITATIONS.....	34
CONCLUSION.....	35
REFERENCES	36

INTRODUCTION

Subjective well-being and major depressive disorder seem to represent two opposites in the study of mental health – one characterised with positive mood states and happiness (SWB) and the other one with negative affect (major depression).

Whereas major depressive disorder (MDD) is one of the most commonly diagnosed mental disorders, with a lifetime prevalence in the United States estimated to be 16.2 % (Kessler et al., 2003), SWB has been regarded as the main psychological construct of happiness. SWB is closely associated with the growing field of positive psychology which has been described as a contemporary reaction to the excessive focus on the negative side of mental health in psychiatry and clinical psychology. For example Seligman and Csikszentmihalyi (2000) have suggested that psychologists should strive to understand what makes life good and not just what makes it bad. To this one could obviously counter that understanding more about disorders will help health professionals of relieving individuals of such.

In this thesis I have tried to explore the etiology and associations between subjective well-being and major depressive disorder, using a twin research paradigm. Twin research may provide some answers to old questions of nature and nurture. In this thesis, my specific aims were to investigate what role genes and environment play in the development of happiness (SWB) and depression (MDD) and whether happiness and depression are caused by the same set of genes and environmental factors.

I will begin this thesis by giving a phenomenological description of subjective well-being and major depressive disorder and a summary of important research findings to date. Next I will provide a short historical introduction to the field of behavioural genetics, followed by a description of the central concepts and assumptions of the twin methodology. The last part of the thesis consists of the present twin study.

Subjective Well-Being

What makes people happy? What is a good life? Are wealthier people happier than the poor? Are people in the countryside happier than people in the urban areas? Questions like these have kept philosophers, economists, psychologists and a wide variety of other disciplines preoccupied for many decades. According to Diener, Lucas and Oishi (2005),

psychologists have studied subjective well-being since the 1920s. In 1967, Warner Wilson concluded from a review of articles of avowed happiness that the happy person “emerges as a young, healthy, well-educated, well-paid, extroverted, optimistic, worry-free, religious, married person, with high self-esteem, high job-morale, modest aspirations, of either sex and of a wide range of intelligence” (Wilson, 1967, p. 294). Psychologists have coined the term Subjective Well-Being (SWB) to reflect what most people think of as happiness. Subjective Well-Being can be defined as a “person’s cognitive and affective evaluations of his or her life” (Diener, Lucas, and Oishi, 2005, p.63).

Diener, Scollon and Lucas (2003) propose a structure of subjective well-being that comprises positive affect, negative affect, global life judgments, and domain satisfaction. Positive and negative affect can be said to be the ability to experience positive emotions and the ability to experience negative emotions, respectively. Some researchers argue that positive affect and negative affect vary independently (Larsen, McGraw, and Cacioppo, 2001; Watson, Kendall, 1989), whereas others argue that positive and negative affect are best captured as one single bipolar dimension (Russel and Carroll, 1999). Diener et al. (2003) notes that positive and negative affect are best measured separately whatever the outcome of the more theoretical discussion will be, because positive and negative affect seems to correlate differently with other constructs. For example Kendall and Watson (1989) showed that depression is characterized by low positive and high negative affect whereas anxiety is characterized by a high negative affect but not a low positive affect.

The third component of the subjective well-being construct is global life satisfaction judgments which reflect a cognitive process in which an individual assesses his or her life in a general (overall) manner. Life satisfaction is a component that according to Pavot and Diener (1993) is clearly separable from the affective components. Pavot and Diener (1993) argue that there are three important ways that life satisfaction measurements differ from the affective components. Firstly, individuals may suppress negative emotional concerns, but still recognize negative factors in a more global manner. Secondly, emotional responses have a short influence whereas a cognitive factor like life satisfaction has a wider perspective and is thus not so biased by the moment. Thirdly, emotional responses may reflect unconscious processes, whereas life satisfaction judgments often reflect goals and values.

The fourth component of SWB is domain satisfaction. This component is thought to reflect the different domains in life that are important to individuals. According to Diener et

al. (2003) this component is thought to be specific for each individual, because different individuals will place different values to different domains according to what one regards as particularly important in life.

The etiology of SWB

Several factors are thought to influence subjective well-being; some of them will be reviewed here. Subjective well-being is a multifactorial concept influenced by several sources; however it seems that in broader time perspective personality and as we shall see genes seems to be the main sources of influence. Costa and McCrae (1980) have shown extraversion and neuroticism to be closely related to subjective well-being, finding that extraversion predict positive affect whereas neuroticism predict negative affect. In a meta-analysis by DeNeve and Cooper (1998) investigating the association between personality traits and subjective well-being, neuroticism was shown to be the strongest predictor of life satisfaction, happiness and negative affect, whereas extraversion and agreeableness predicted positive affect equally well.

Life events may also influence subjective well-being. However, the effect of life events on SWB has been shown to be mainly short-term. Suh, Diener, and Fujita (1996) found that only recent life events matter, showing the impact of most life events on subjective well-being to be very small after a period of up to 3 months. Some life events may have more long-lasting impact however. For example Hansson, Forsell, Hochwälder, and Hillerås (2008) reported that respondents reported less subjective well-being at three year follow up when their financial situation had worsened, or their civil status or social support level had changed, Income and subjective well-being was also reported by Diener, Sandvik, Seidlitz, and Diener (1993) to relate to SWB in a curvilinear fashion. This means that subjective well-being increases up to a certain income point where the increase in subjective well-being diminishes for each increase in income.

Genetics is likely to be an important factor in determining subjective well-being. There has been a growing understanding of the genetic basis for subjective well-being over the last 10-20 years and a number of twin studies have been published. According to a review by Nes (2009), studies examining heritability, or time specific influences from genetic factors on subjective well-being commonly estimate the genetic influence to explain 35%-50% of the variance in SWB. Worth noting, however, is that some studies find the genetic basis of subjective well-being to be best understood by an additive genetic model (e.g. Røysamb,

Harris, Magnus, Vittersø, and Tambs, 2002), while other studies report mainly non-additive genetic effects (dominance, epistasis) on subjective well-being (Stubbe, Posthuma, Boomsma, and De Geus 2005; Tellegen et al., 1988).

One of the intriguing opportunities generated by the increased research in to this field and developments in methodology is the opportunity to look at both the time specific and stable genetic and environmental basis for subjective well-being. This is made possible due to the longitudinal twin designs employed by some researchers. Time specific genetic estimates (heritability) of subjective well-being have been investigated in many studies using somewhat different measurement instruments (i.e. well-being questionnaires). Studies that have investigated the genetic basis of a more stable subjective well-being construct are few. Lykken and Tellegen (1996) administered the Well-Being scale of the Multidimensional Personality Questionnaire to 2310 twins. The authors found that educational level accounted for less than 2% in women (less than 1% in men), socioeconomic status similarly accounted for less than 2%, and income accounted for less than 2% of the variance (Lykken and Tellegen, 1996). When administering the same questionnaire to 79 monozygotic (MZ) twins and 48 dizygotic (DZ) young adult co-twins with ten years between the two test rounds, they found that the cross-twin cross-time correlations (i.e. the correlation between twin 1 at time 1 and twin 2 at time 2) were almost zero for DZ twins, whereas the MZ cross-twin cross-time correlation was 0.40 (i.e. explaining 80% of the variance). This means that in a 10 year perspective 80% of the variance in well-being levels is attributable to genetic influence (Lykken and Tellegen, 1996). Nes, Røysamb, Tambs, Harris, and Reichborn-Kjennerud (2006) investigated subjective well-being in a longitudinal twin design using two assessments (6 years between measurement occasions). Their analysis showed that additive genetic influence could explain 81% of the variance in male's subjective well-being and 75% of the variance in female's subjective well-being over the two measurements. The remaining variance was explained by the non-shared environment. Both Lykken and Tellegen (1996) and Nes et al. (2006) thus clearly show that the stability in subjective well-being is much due to genetic influences.

Given this stable genetic basis for subjective well-being, and the fact that subjective well-being is highly correlated with other positive phenotypes such as high extraversion, conscientiousness and low neuroticism (Weiss, Bates, and Luciano 2008), and perceived health (Røysamb, Tambs, Reichborn-Kjennerud, Neale, and Harris 2003), Weiss, King and

Enns (2002) coined the term covitality (as opposed to comorbidity) to reflect that subjective well-being is correlated with other positive phenotypes, this will be discussed later.

Major Depression

Depression is one of the most commonly diagnosed psychiatric disorders, with an estimated lifetime prevalence at 17.8 % for people aged 18 to 65 and living in the Oslo region (Kringlen, Torgersen and Cramer, 2001). As a comparison, the lifetime prevalence for major depression in the National Institute Public Health Twin Panel was estimated to be 14% (Mykletun, Knudsen, and Schjelderup Mathiesen, 2009). Some of the symptoms that characterize depression include depressed mood, sleep problems, weight gain or loss, feelings of guilt, worthlessness, and a wide variety of other symptoms. Depressive disorders include major depressive disorder, dysthymic disorder, and depressive disorder not otherwise specified (NOS). To qualify for a diagnosis of major depression one has to have five or more of the following symptoms:

- 1. Depressed mood most of the day or nearly every day, as indicated by either subjective report (e.g., feels sad or empty) or observation made by others (e.g., appears tearful). Note: In children and adolescents can be irritable mood.;*
- 2. Markedly diminished interest or pleasure in all, or almost all activities most of the day, nearly every day (as indicated by either subjective account or observation made by others);*
- 3. Significant weight loss when not dieting or weight gain (e.g., a change of more than 5% of body weight in a month), or decrease or increase in appetite nearly every day. Note: In children, consider failure to make expected weight gains;*
- 4. Insomnia or hypersomnia nearly every day;*
- 5. Psychomotor agitation or retardation nearly every day (observable by others, not merely subjective feelings of restlessness or being slowed down);*
- 6. Fatigue or loss of energy nearly every day;*

7. *Feelings of worthlessness or excessive or inappropriate guilt (which may be delusional) nearly every day (not merely self-reproach or guilt about being sick);*
8. *Diminished ability to think or concentrate, or indecisiveness, nearly every day (either by subjective account or as observed by others);*
9. *Recurrent thoughts of death (not just fear of dying), recurrent suicidal ideation without a specific plan, or a suicide attempt or a specific plan for committing suicide.* (American Psychiatric Association, DSM-IV-TR, 2000, p. 356).

The etiology of Major depression

The etiology of depression is multifactorial and the causal pathways are complicated. There are a number of perspectives aiming to explain the etiology of major depression. The psychological approach has not been a unified one, being characterized by several different schools of thought. The psychodynamic perspective on the etiology has focused on the presence of unconscious motivation and conflicts, whereas the cognitive perspective has emphasized errors in logic and attribution (Seligman, Walker, and Rosenhan, 2001). The biological approach, usually portrayed as an alternative rather than integrative view to the psychological approach, combines information about genes and modern neuroscience, including biochemistry.

The twin method has been successful in showing that variance in the different depressive phenotypes (i.e. disorders as well as sub-diagnostic conditions) can be attributed to both genetic and environmental factors. What are the results of twin, family and adoption studies for depression? Sullivan, Neale and Kendler (2000) conducted a meta-analysis where they looked at five family studies, three adoption studies and six twin studies.

The five family studies all showed increased risk for major depression in first degree relative versus comparison subjects (Sullivan et al., 2000). Family studies included in this meta-analysis did not permit the opportunity to distinguish between genetic and environmental influence. To shed light on this one have to look at the twin and adoption studies.

Although none of the adoption studies met the authors' inclusion criteria, they reviewed three adoption studies qualitatively. Adoption studies are generally associated with a number of methodological difficulties, for example representativeness and privacy protection (Plomin, DeFries, McClearn, and McGuffin, 2008). The authors argue that the findings from early adoption studies are important because there may not be many adoption studies in the future (Sullivan et al., 2000) and conclude that two out of three adoption studies indicate genetic influences on major depression. The study that did not support this notion used sources to verify depression diagnoses that may underestimate the lifetime prevalence of depression (Sullivan et al., 2000).

Six twin studies were included in the meta-analysis and all of them showed considerable genetic influences on major depression. The authors concluded that the heritability for major depression is in the range of 31%-42%. The authors note, however, that this might be an underestimate of the true heritability estimate, because of the sometimes unreliable diagnosing of major depression (Sullivan et al., 2000). Thus there seems to be a significant portion of the variance attributable to genetic factors in the etiology of depression and a substantial portion being due to the non-shared environment.

Several specific environmental vulnerability factors have been identified as important in the development of depression. Socioeconomic Status (SES) has for example been found to be an important factor in the etiology of depression. In a meta-analysis by Lorant et al. (2003) consisting of more than 50 studies of depression, the authors concluded that socioeconomic status slightly increases the risk for onset of depression, but the risk for staying depressed are even higher in low socioeconomic groups. The authors also note that one can follow these differences throughout the entire social spectrum. This means that the difference is not just observable in the lowest socioeconomic groups versus the highest socioeconomic group, but that differences in socioeconomic status can be observed at more subtle levels.

The experience of stressful life events may also be related to the onset of major depression. Along with SES, the impact of some life events may, however, partly be related to genetic liability (Kendler et al., 1995). Moderation of stressful life events have been linked to different variations of the 5-HTT gene which are involved in the regulation of serotonin (Caspi et al., 2003). This promising finding has however failed to be replicated one study and been partially replicated in another study (Gillespie, Whitfield, Williams, Heath, and Martin, 2005; Kendler, Kuhn, Vittum, Prescott, and Riley, 2005).

Differences in personality makeup also seem to be of interest in understanding the course and outcome of major depression. High trait levels of neuroticism seems to increase the risk for lifetime depression, while high trait levels of extraversion seems to decrease the risk for lifetime depression (Kendler, Gatz, Gardner, and Pedersen, 2006). Studies of the harm-avoidance and self-directedness traits have also been shown to predict vulnerability to depression (Cloninger, Svrakic, Przybeck, 2006).

A central characteristic of the depression disorder is its high comorbidity rate, this means that a person with a depression disorder has at least one other disorder. Findings from the National Comorbidity Study Replicated (NCS-R) showed that 72.1 % of individuals with a lifetime major depressive disorder also had at least one comorbid disorder, with anxiety disorder as the most common comorbid disorder (Kessler et al. 2003). Part of the reason for this can be the fact that the inclusion criterion for depression in DSM-IV is so wide that a lot of people will have enough symptoms to qualify for the depression diagnoses (Kessler et al., 2003). Mineka, Watson and Clarke (1998) discuss whether the position that psychiatric disorders can be viewed as “distinct clinical entities” (p. 380) have gone too far. They argue that because of the high comorbidity rate for disorders, a more unified view is needed. The liability spectrum model proposed by Krueger and Markon (2006) proposes a view where psychiatric disorders are viewed as sub dimensions of higher order factors. There are two main factors in this model being internalizing and externalizing disorder. Internalizing disorders can be further divided into distress and fear. Distress comprises of major depression, dysthymia and generalized anxiety disorder. Fear includes phobias and panic disorder. Externalizing disorders are alcohol disorder, drug disorder, conduct disorder and adult antisocial behavior. Kendler, Prescott, Myers, and Neale (2003) tested this structure using twin methodology. The structure of this model was replicated yielding a specific genetic influence for the internalizing disorders, a specific genetic influence for externalizing disorders and specific genetic influence of alcohol dependence and drug dependence (Kendler et al. 2003). The factor structure was only replicated with genetic influence. The results might explain the high comorbidity rates seen for several psychiatric disorders, as the same genes might cause the same disorders. The results indicate that there is a more general genetic liability to psychiatric disorders; this might explain some part of the comorbidity problem in classifying psychiatric disorders.

Behavior Genetics

A Brief History

The foundation for behavioral genetics was laid out in the 19th century by several seminal figures in the history of science. Gregor Mendel discovered the basic principles of heredity through experiments with pea plants, Charles Darwin issued *On The Origin of Species by Means of Natural Selection* in 1859, and Francis Galton (Darwin's cousin) published studies of how intelligence is inherited. These three important scientific milestones were not immediately identified as works that could pull in the same direction however. According to Morrison (2002) the debate in the UK in the early part of the 20th century where between the advocates of the Mendelian school of thought (mendelians) and people using statistical methods to investigate traits and heredity (biometricians) mainly influenced by Darwin, and to some extent Francis Galton. The debate centered around the disagreement of whether complex traits could be described as single gene effects and whether Mendel's laws were applicable to statistical methods (Plomin et al., 2008). In 1918 Ronald Fisher published a paper called "The Correlation between Relatives on the Supposition of Mendelian Inheritance". This paper is usually considered to have "resolved" the battle between mendelians and biometricians (Morrison 2002).

From the 1950s and to the present time, behavior genetics and biologically founded explanation models have varied in strength and influence. The discovery of the DNA molecule in 1953 by Watson and Crick set the stage for a deeper understanding of how genetic influences are transmitted from one generation to another. When the DNA was discovered, psychology was in a stage of what Rutter, Moffitt, and Caspi (2006) calls "extreme environmentalism" (p.226). This can partly be explained by the impact of several dominating "schools of thought" within psychology, such as behaviorism that considered stimulus and response patterns as the main interest for study. Behaviorism viewed the child as a tabula rasa. An opposing view came from developmental psychologist such as Mary Ainsworth and John Bowlby who claimed that a child was born into the world with several innate "attachment programs". Their focus was more towards parent and parent behavior, however, with Ainsworth stressing the importance that parents create a secure base. In 1968 R. Q. Bell wrote an important paper in which he challenged the prevailing view that the relationship between parent and child is unidirectional, arguing that parents change their

behavior according to the child's behavior (i.e. the child evoke certain behavior in the parents).

Although the 50s and the 60s can be labeled a period of extreme environmentalism, this period saw the release of the first textbook in behavioral genetics called *Behavioral Genetics* by John Fuller and Robert Thomson (Baker, 2007). In 1970 the Journal of Behavior Genetics was founded and is one of the most important journals for publishing research on behavior genetics today (Baker, 2007). Rutter et al. (2006) sums up the period from 1960-1980 as a period of substantial growth in genetic research and consider the period from 1980 to the early 1990s as a period in which the environment was neglected. This is perhaps one of the reasons why there have been several outspoken critics against research concerning genetics in relationship with psychology, such as Jay Joseph (2004). Part of the reason for this may be that some schools in psychology have been used to view individuals as products of their environment and to a lesser degree a product of their biologic makeup. Some psychologist (and other scholars) thus feels that genetics can shift the centre of gravity from an emphasis on the environment to an emphasis on biology; biological explanations to human behavior might be seen by some as a more deterministic view of man.

Important concepts in behavior genetics

Twin studies estimate the contribution from genes and environments to a given phenotype. Environmental effects are split into shared (*c*) and non-shared (*e*) effects. Genetic effects are split into additive (*a*) and non-additive effects (*d*). In the next section I will give a thorough presentation of what environmental and genetic influences is in twin research.

Genetic Effects

A gene is a sequence of the DNA molecule which can be located at the chromosomes in every human cell. A gene is in biometrical genetics commonly defined as a “unit factor of inheritance” (Neale and Maes, 2000, p.55). The location of a gene on the chromosome is called a locus, and alternative forms of a gene that are located on the same locus are referred to as alleles (Neale and Maes, 2000). The genotype “is the chromosomal complement of alleles for an individual” (Neale and Maes, 2000, p.55). The phenotype is the observable characteristics. Genetic effects can be either additive or non-additive. The additive genetic factor (denoted *A* in twin modeling) are defined as the “sum of the average effects of the individual alleles” (Neale and Maes, 2000, p.56).

In the Mendelian school alleles are often symbolized with capital letters (A) meaning dominant gene and small letter (a) meaning recessive gene. A two allele system can be said to be homozygote if both the alleles on a locus is either recessive (aa) or dominant (AA), and heterozygote if one of the alleles are dominant and the other recessive (Aa). (Neale and Maes, 2000).

The biometrical approach for calculating heritability estimates assumes a polygenic model, meaning that a large number of genes are causing variation in phenotypes (Neale and Maes, 2000). The additive genetic influence that is calculated in twin modeling is a measure of average effect of the individual alleles (Neale and Maes, 2000). Non-additive genetic effects reflect interaction between alleles – either at the same locus (dominance) or between loci (epistasis) (Purcell, 2008).

Heritability (h^2) is defined as “... the proportion of phenotypic variance that can be accounted for by genetic differences among individuals” (Plomin et. al 2008, p. 83). Heritability is commonly divided into broad heritability and narrow heritability (Plomin et al., 2008; Neale and Maes, 2000). Narrow heritability refers to a heritability estimate which only accounts for the additive genetic effects. Broad heritability, which is most commonly used under ‘heritability’, takes all genetic effects into account (i.e. both additive and non-additive effects). Heritability is an often misused and misunderstood concept. Part of this misunderstanding refers to the fact that heritability estimates concerns a given population, not single individuals. Another misunderstanding is that heritability estimates are an exact and constant number. Heritability estimates concerns a specified population at a particular time, this means that if the genetic makeup of this population were to change (as it likely will when time goes by) heritability estimates will change.

Environmental Effects

In twin modeling the shared environment is a broad concept that refers to all environmental effects that co-twins share (i.e. it refers to all non-genetic influences that make family members similar) (Neale and Maes, 2000). The non-shared environment refers to environmental influences that contribute to differences between co-twins (Neale and Maes, 2000). In classical twin modeling, the shared environment is denoted C (common) whereas the non-shared environment is denoted E. The non-shared environment is computed as a residual term after the genetic variance and the shared environment have been accounted for. This implies that measurement error will be grouped together with the non-shared

environmental factor, consequently resulting in overestimation of the non-shared environment and underestimation of heritability.

An important distinction in relation to the shared and the non-shared environment is the distinction between objective and effective environments. According to Turkheimer and Waldron (2000), objective environments “refer to environmental events as they might be observed by a researcher, as opposed to how they affect family members” (p. 79). By contrast, effective environments “are defined by the outcomes they produce” (Turkheimer and Waldron, 2000, p.79). Many psychologists and social scientists have been surprised, and some probably also disappointed, by the fact that twin research often does not find a significant shared environmental component. This may be due to the fact that twin modeling only measures the effective environment (i.e. the effect of the environment). An objective event that affects both twins (e.g. a divorce) may have different effect on the twins creating differences between them and thus being loaded on to the non-shared environmental factor and not the shared environment factor.

One way to assume that there is a substantial shared environmental component is if the correlation matrix suggest so, if shared environment were present one would predict that dizygotic correlations would be closer to monozygotic correlations than one could expect from genetic influence (i.e. more than half the size of monozygotic correlations). One of the drawbacks with the shared environmental concept as it is used, is that one cannot separate between different sources of shared environment, thus finding that shared environment is of great importance for a trait does not give any insight into what kind of environmental influence that might be.

Genotype- Environment Interplay

According to Neale and Maes (2000) there are three conditions in which there are genotype- environment effects that need to be considered; the first being assortative mating, the second being genotype environment correlation and the third being genotype by environment interaction (G x E). Assortative mating will be described later under Twin Method Assumptions (page 18).

The first type of genotype-environment effect is the so-called genotype-environment correlation (CorGE). Quantitative genetics have made several important discoveries about the genetic basis of psychological traits and disorders, but it has also made important discoveries

about the genetic influence on the environment. According to Plomin et al. (2008) there are three types of genotype-environment correlation: passive, evocative and active.

Passive genotype- environment correlation refers to the fact that children are brought up in an environment which are created by their parents which they are genetically correlated with (Plomin et al. 2008). A common example of this is that children with intelligent parents often are brought up in an intellectually stimulating environment, thus being able to nurture their cognitive abilities.

Evocative genotype- environment correlation occurs when the genetic makeup of individuals causes reactions in others (Plomin et al. 2008). Some people have attributes that lets them go through life causing less stir and commotion than others. Reactions by the environment that are caused in some degree by the genetic makeup of a person are the essential feature of this interaction (Kendler and Prescott, 2006)

Active genotype-environment effects are when individuals create their own environment by selecting friends, hobbies and creating experiences that are correlated with their genetic makeup (Plomin et al. 2008). This is also called genotype environment autocorrelation (Neale and Maes 2000).

The second type of genotype- environment effects are the genotype by environment interaction (G x E) (Kendler and Prescott, 2006; Neale and Maes, 2000). Broadly speaking, G x E occurs either i) when genes alter the person's sensitivity to specific environmental features, or ii) when environmental contexts differentially modify genetic effects (i.e. genetic dispositions are expressed differently in different environments). Genotype by environment interaction does not refer to any volitional action by the individual on the environment like the active genotype-environment correlation.

Neale and Maes (2000) makes a distinction between scalar and non-scalar G x E. Scalar G x E means that "the same genes are expressed consistently at all levels of a salient environmental variable so that only the amount of genetic variance changes between environments" (Neale and Maes 2000, p. 23). Non-scalar G x E means that different genes are expressed in different environments (Neale and Maes, 2000).

Twin Method Assumptions - Assortative Mating

According to Neale and Maes (2000): “any non-random pairing of mates on the basis of factors other than biological relatedness is subsumed under the general category of assortative mating” (p. 18). Twin research relies on the assumption that there is random mating and not assortative mating. According to Kendler and Prescott (2006), however, the critical assumption is not whether couples have the same education or whether they earn the same amount of money, the essential thing is whether they differ more or less in genetic liability to the trait under study. This is thought to have implications for twin research (i.e. the heritability estimates may be uncertain). In short, the twin method relies on the basis that monozygotic twins share all their genes and dizygotic twins share half of their genes. If one assumes that a trait has some genetic basis one can look at the difference between monozygotic and dizygotic twins and calculate a genetic component. However, in the case of assortative mating, dizygotic twins will possibly share more than 50% of their genes. This will result in reduced heritability estimates and increased estimates of the shared environmental component in the classical twin study (Kendler and Prescott, 2006).

Twin Method Assumptions - The Equal Environment Assumption (EEA)

As previously stated, the twin method assumes that monozygotic co-twins are identical in their genetic makeup whereas dizygotic twins share on average 50% of their genes. Thus, to estimate the genetic influence on a trait or disorder, one looks at the difference in correlations between monozygotic and dizygotic co-twins. What if this difference is not due to genetic differences, but rather due to monozygotic twins experiencing a more similar environment? Monozygotic twins are for example more likely to be dressed alike, play together (6-12 years), and spend time together (12-18 years) than are dizygotic co-twins (Loehlin and Nichols, 1976). The equal environment assumption states that “... DZ twins, between them, share environmental influences to the same degree as do MZ twins” (Beckwith, 2006, p. 78). The equal environment assumption concerns whether monozygotic twins experiencing more “twin characteristic” environment makes their liability for major depression or any phenotype/trait any different than dizygotic twins. According to Kendler and Prescott (2003) there is not a straight forward answer to this as they state “there is no such thing as a generic violation of the EEA” (p.116). What they mean by this is that one has to test whether there could be a violation of the equal environment assumption for the particular trait or disorder under study.

A recent study examining the equal environment assumption by Johnson, Krueger, Bouchard Jr, and McGue (2002) investigated if the personalities of twins are different from that of singletons. Monozygotic twins, dizygotic twins, and singletons were compared on the Multidimensional Personality Questionnaire (MPQ) (Johnson et al., 2002). Only trivial differences were found, with the exception of social closeness, this had however no effect on the higher order factor of positive emotionality that social closeness contributes to (Johnson et al., 2002). The authors thus conclude that differences in personality makeup will not affect subsequent studies (Johnson et al. 2002).

The equal environment assumption has also been tested specifically for psychiatric disorders. Kendler and Gardner (1998) interviewed female-female twins from the Virginia Twin Registry, assessing a variety of psychiatric disorders including major depression. The twins were also interviewed on childhood and adolescence experiences, treatment from environment, and their relationship with the other twin (Kendler, and Gardner, 1998). A factor analysis resulted in three factors which were examined in relation to the psychiatric disorders. These were; childhood treatment, co-socialization, and similitude (to which degree twins and themselves emphasized similarities) (Kendler, and Gardner, 1998). None of these factors predicted psychiatric disorders, with the exception of broadly defined bulimia. The results thus point in the direction that equal environment assumption will not be violated when examining psychiatric disorders from a behavioural genetic perspective.

Genetic Epidemiology and Psychiatric Genetics

In this section I will give a presentation of what genetic epidemiology and psychiatric genetics is, and what implications it has for twin research. Genetic epidemiology can be said to be: "... the study of the role of genetic factors and their interaction with environmental factors in the occurrence of disease in human populations" (Khoury, Beaty, and Cohen, 1993, p.13). Most diseases fall in a multifactorial category, resulting from a complex interplay of biological, social and psychological risk factors (Khoury et al., 1993).

Genetic epidemiology and psychiatric genetics can be viewed as partly overlapping disciplines where the latter focuses exclusively on psychiatric disorders. Psychiatric genetics can be divided into four paradigms; basic and advanced genetic epidemiology, gene finding, and molecular genetics (Kendler, 2005). According to Kendler (2005) the heritability estimates and the way in which heritability is calculated and conceptualized is both the strength and weakness of basic and advanced genetic epidemiology. Regarding the positive,

establishing heritability estimates for a disorder is in itself important. As Kendler (2005) notes establishing heritability can spur on future research and give credence to research looking for specific genes that increases liability to disorders. The limited versatility of the heritability concept described earlier is however seen as a disadvantage (Kendler, 2005). Another disadvantage is the liability threshold model, which assumes that genetic liability is normally distributed in the population (Plomin et al. 2008). According to Kendler (2005) this liability threshold model can be quite different from actual biological processes. Basic and advanced genetic epidemiology shares many of the strengths and weaknesses, however advanced genetic epidemiology tries to go a step further and describe the causal pathways, whereas basic genetic epidemiology is descriptive (Kendler, 2005).

METHODS

Sample

The present study is based on the National Public Health Institute Twin Panel. The twin panel consists of information from 15,370 twins born between 1967 and 1979 (Harris, Magnus, and Tambs, 2002). The twin panel consists of information from the medical birth registry, longitudinal data, DNA, and sub-studies (Harris et al., 2002). This paper will focus on longitudinal data, which consists of two self report questionnaire surveys known as Q1 (1992) and Q2 (1998) and an interview assessment conducted 1999-2003.

Self report questionnaire 1 (Q1) was mailed out to all twins born between 1967 and 1974, with a Norwegian address, 18 years and older, in 1992. Q1 was sent out by mail to 3996 pairs (7,992 individuals in total), 2,570 complete pairs and 724 singletons responded to this questionnaire (Harris et al., 2002). The second questionnaire (Q2) was sent out to the cohort that received the Q1, and to twins born up until 1979 (Harris et al., 2002). In total 6,349 pairs received Q2, 3,334 complete pairs responded and 1,377 singletons responded. This yields a participation rate for Q1 of 65% and 53% for Q2. The drop in participation rate can be attributed to several factors for example Q1 had fewer questions than Q2. According to Harris et al. (2002) there seems to be a general trend that it is harder to get people to participate in surveys. All pairs that had completed Q2 were invited to participate in the mental health interview study that took part between 1999 and 2004. This interview consisted of two parts. The first part the Munich-Composite International Diagnostic Interview (M-CIDI) was administered. This interview assesses DSM-IV axis 1 and ICD 10 life time diagnoses (Tambs,

et al., 2009). The second part consisted of the Structured Interview for DSM-IV Personality (SIDP-IV), which assesses axis 2 personality disorders (Tambs et.al., 2009).

In this present study, SWB data from 2513 twin pairs and 774 singletons responding to the Q1 and SWB data from 3286 twin pairs and 1399 singletons participating in Q2, were analyzed. The interview data being analyzed consisted of 1383 complete twin pairs and 22 singletons.

Measures

Subjective well-being was measured on a 3 item scale comprising one life satisfaction item; “When you think about your life at present, would you say that you are mostly satisfied with your life, or mostly dissatisfied? Participants responded on a scale from “extremely satisfied” to “very satisfied”, there were 6 response categories. The two other items intended to measure positive and negative affect. The first one being “Are you usually happy or dejected?” participants had 5 response categories ranging from “dejected” to “happy”. “The second one being “Do you usually feel strong and fit or tired and worn-down?” participants had 4 response categories ranging from “very strong and fit” to “tired and worn-down”. Because each item had a different number of response categories, all items were transformed to a 0-10 scale. This was done by using the transformation algorithm: $X = (Y - 1) \times 10 / (Z - 1)$ where X is the new score, Y the original score and Z the number of response categories. The transformed variables were summed, and an ordinal SWB variable ranging from zero to five was subsequently constructed by imposing thresholds based equally spaced percentiles of the distribution. This is equivalent to what Røysamb et al. (2003) and Nes et al. (2006) previously has done. The SWB index used in these previous studies included 4 items, however, of which 3 were identical to the items used here. In this study, we excluded one item measuring negative affect (nervousness). Cronbach`s alpha was estimated to be 0.64 and 0.67 for the Q1 and Q2 data.

Major depressive disorder was measured by a psychiatric interview known as M-CIDI which is a computer aided version of the WHO CIDI (Wittchen, Lachner, Wunderlich, and Pfister, 1998). CIDI measures all DSM-IV axis 1 disorders and ICD 10 lifetime diagnoses. M-CIDI has been shown to have good test retest reliability (Wittchen et al., 1998).

In this paper the latent subjective well-being concept has been fitted to what is known as a common pathway model (figure. 1). The common pathway model assumes that the

common genetic and environmental influence load onto a latent variable (Purcell, 2008). The thought here is to use both measurements and “extract” the stable SWB component. The advantage by doing this is that one ends up with a purer subjective well-being concept. This also means that the two measurements end up with some residual variance that cannot be accounted for by a latent variable (these are the separate ACE that SWB Q1 and SWB Q2 has in figure 1). The full trivariate model (figure. 2) is a hybrid model where the correlations between MDD and SWB could be said to resemble that of a correlated factor model and the latent SWB construct are a common pathway model. Here major depressive disorder loads onto a latent variable which essentially are the same as the measured. Some of the interesting things this model can explain are the double headed arrow from ACE of the subjective well-being concept to the ACE of the major depressive disorder variable. This will be discussed later.

Figure 1.

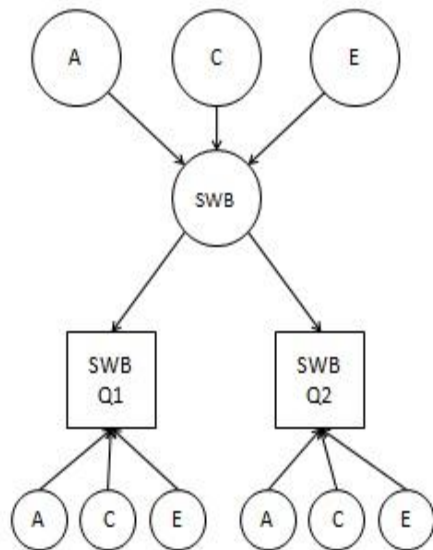
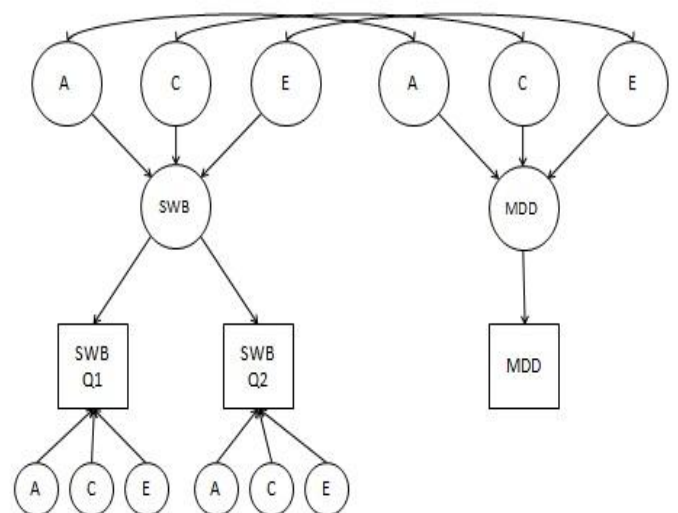


Figure 2.



Statistical analysis

Descriptive statistics were calculated using SPSS, while all structural equation modeling was fitted in Mx. Mx is a free software package developed by Mike Neale specifically for twin studies and the program allows for raw data analyses. The raw data

approach has the advantage of permitting use of all existing data; this means that twins missing some data points or questionnaires can still be used for the analysis. When analyzing raw data Mx use an estimation procedure known as full information maximum likelihood (FIML). In short this estimation procedure calculates a probability score in relation to how probable this particular data point is according to the pre-specified model. The sum of this probability score is known as the -2 times logarithmic likelihood (-2LL). The difference in -2LL is thought to be chi squared distributed with degrees of freedom equal to the difference in number of parameters, although this is widely used, a recent publication has shown that the p-value is somewhat lower, and that model selection should not be based solely on the p-value (Dominicus, Skrondal, Gjessing, Pedersen, and Palmgren, 2006). Mx does not yield an overall goodness of fit index for the full saturated model, only for the nested submodels. Model selection is based on chi square and Akaikes Information Criterion (AIC). AIC is computed using the algorithm $\Delta\chi^2 - \Delta 2df$, the sub model with the lowest AIC is preferred.

Liability threshold model was assumed, meaning that scores on both our phenotypes are presumed to be normally distributed within the population. For subjective well-being this means that a scoring in one of the five categories is thought to be normally distributed, thresholds are modeled to represent these categories. For major depressive disorder this means that the liability for developing MDD is normally distributed and that threshold represent this liability.

A univariate analysis is a testing of how a single phenotype fits different ACE models. Univariate analyses were carried out for the different phenotypes (SWB_{Q1}, SWB_{Q2} and MDD) before proceeding to more complex multivariate analysis. According to Neale and Maes (2000) there are essentially 5 aspects that are tested in a univariate analysis. The first model being tested is usually a full ACE model. This predicts that sources of variance are attributable to additive genetic effects, shared environmental effects, and unique environmental effects. In nested sub models parameters are dropped and tested for significant reduction in fit. In the second model, the C parameter is dropped, resulting in an AE model. This suggests that phenotypic resemblances in twins are due to additive genetic factors and unique environmental factors. The third model being tested is a CE model; this model predicts no genetic influence of the phenotype under study. A correlation pattern that can suggest such a model is when dizygotic correlations are higher than a half of what the monozygotic correlations are. The last model being tested is a pure E model. This suggests that the phenotype under study is purely caused by unique environmental influence.

Structural Equation Modeling

This section will give a brief overview of the methodology necessary for understanding twin modeling, and behavioral genetic research. This includes a brief historical note of the structural equation modeling (SEM) tradition, the computing and rationale behind the variance covariance matrices used in twin modeling, path analysis, model fitting procedures, and the different approaches to multivariate analysis.

Structural equation modeling is in short a set of techniques for fitting observed data to a prespecified model. According to Bollen (1989) there are three important components that helped pave the way for the structural equation modeling tradition that spawned during the late 1960s and early 1970s. These three components are (1) path analysis, (2) latent variable and measurement model, and (3) estimation procedures. Path analysis will be covered in detail later, but at this point it is sufficient to say that Sewall Wright is its founder (Bollen 1989). The tracing rules and principles he developed in the early 20th century are still widely used and is a fundamental component of structural equation modeling tradition (Bollen, 1989). Latent variables and measurement theory are essential in structural equation modeling. Latent variable is a variable that is unobserved, but inferred through a set of observed indicators. The development of factor analysis was an important step in the development of structural equation modeling (Bollen, 1989). Statistical estimation approaches refer to procedures that minimize the difference between observed data and the data that fits the prespecified model. Popular estimation procedures include weighted least square used on a correlation matrix, or as in this paper a full information maximum likelihood estimation used on raw data.

Variance Component

The approach described in the next section is called the variance components approach (Purcell, 2008). In short variance components approach is basically breaking observed variance into different components, in our case this will mean breaking observed variance down to genetic and environmental variance. Genetic and environmental influence on a phenotype can be expressed as:

$$1. \quad P = G + E$$

This can be further broken down as (recall that A is additive genetic contribution, C is shared environmental influence, and E is non-shared environmental influence):

$$2. \text{Var} (P) = \text{Var} (A + C + E)$$

The formula for calculating the variance of a sum is:

$$3. \text{Var} (X) = \text{Var} (X) + \text{Var} (Y) + 2\text{cov} (X,Y)$$

This expression used on our formula for calculating genetic and environmental influence on phenotype yields:

$$4. \text{Var} (P) = \text{Var} (A) + \text{Var} (C) + \text{Var} (E) + 2\text{cov} (A,C) + 2\text{cov} (A,E) + 2\text{cov} (C,E)$$

Here all the covariance expressions are theoretically assumed to be zero. First it is assumed that there is no covariance between genetic effects and either the shared environment or the non-shared environment (Purcell, 2008). As discussed earlier this is a rationale that probably not holds true. The covariance between shared and non-shared environment are also assumed to be zero (Purcell, 2008). Hence the variation at a phenotype can be expressed as:

$$5. \text{Var} (P) = \text{Var} (A) + \text{Var} (C) + \text{Var} (E)$$

Based on the observed data, a covariance matrix can be calculated, the covariance matrix for monozygotic twins is shown in the matrix below. Position (1,1) and (2,2) contains the variance for each twin, whereas position (2,1) and (1,2) contains the covariance between each twin. Consequently the covariance matrix for monozygotic and dizygotic twins will look as this (Purcell, 2008, p.385):

$$6. \begin{bmatrix} \text{Var}MZ^1 & \text{Cov}MZ^{21} \\ \text{Cov}MZ^{12} & \text{Var}MZ^2 \end{bmatrix} \quad \begin{bmatrix} \text{Var}DZ^1 & \text{Cov}DZ^{21} \\ \text{Cov}DZ^{12} & \text{Var}DZ^2 \end{bmatrix}$$

The variance expression in position (1,1) and (2,2) are the expression outlined in (2).

Monozygotic twins are thought to share all their genes whereas dizygotic share half of their genetic makeup. Shared environment are thought to be shared equally for both zygosity groups, whereas non-shared environment is as the name implies not shared by neither monozygotic nor dizygotic the covariance expression in position (1,2) and (2,1) thus yields:

$$7. \text{Cov} (P_{MZ}) = \text{Var} (A) + \text{Var} (C)$$

And for dizygotic twins:

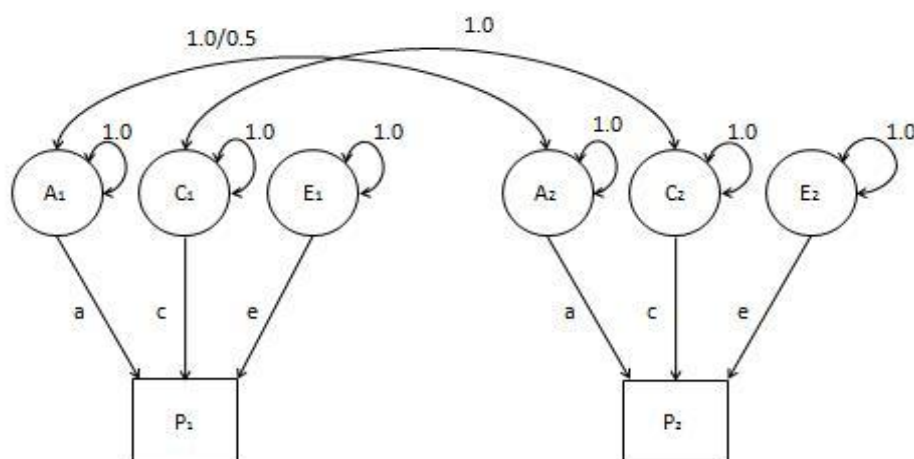
$$8. \text{Cov} (P_{DZ}) = \frac{1}{2} \text{Var} (A) + \text{Var} (C)$$

Path Analysis

A path diagram is a way of expressing a set of equations using arrows, circles and squares. A path diagram will for a lot of people be easier to interpret than a set of equations. There are stringent rules largely developed by Sewall Wright for how a path diagram should be presented. The classical twin model in figure 3 may serve as an illustration. In path diagram latent or unobserved variables are presented as circles (Bollen, 1989). Square boxes represent observed variables; in the classical twin model this will mean the observed phenotype of a twin. A single headed arrow means that variable being pointed at is caused by the variable not being pointed at (Bollen, 1989). While a curved double headed arrow means that there are unanalyzed associations between the two variables (Bollen, 1989). Since monozygotic share all of their genes and dizygotic twins share half of their genes, thus the double headed arrow between A_1 and A_2 will either have the value 1 or 0.5. The shared environment is assumed to be the same for monozygotic twins as well as for dizygotic twins thus C_1 and C_2 correlation is 1. Tracing rules in path analysis is a set of rules that when applied right yields the expected variances and covariances. According to Neale and Maes (2000, p. 92) there are three tracing rules for standardized variables, these are:

- “1. Trace backwards along an arrow and then forward or simply forwards from one variable to the other but never forward and then back.*
- 2. Pass through each variable only once in each chain of paths.*
- 3. Trace through at most one two-way arrow in each chain of paths.”*

Figure 3 (Purcell, 2008, p. 392).



By using these three rules one can calculate both the expected variance and covariance expressions for both monozygotic and dizygotic twins. Monozygotic and dizygotic twins variance (i.e. what is will cause variation in each twin) will be (Purcell, 2008, p.393):

$$9. (a \times 1.0 \times a) + (c \times 1.0 \times c) + (e \times 1.0 \times e) = a^2 + c^2 + e^2$$

To calculate the covariance for monozygotic twins one can only go through the arrows that the two twins share thus yielding (Purcell, 2008, p.393):

$$10. (a \times 1.0 \times a) + (c \times 1.0 \times c) = a^2 + c^2$$

The covariance expression for dizygotic twins equals (Purcell, 2008, p.393):

$$11. (a \times 0.5 \times a) + (c \times 1.0 \times c) = \frac{1}{2} a^2 + c^2$$

This yields the full variance covariance matrix for monozygotic twins that are used in the analysis:

$$12. \begin{bmatrix} a^2 + c^2 + e^2 & a^2 + c^2 \\ a^2 + c^2 & a^2 + c^2 + e^2 \end{bmatrix}$$

And the following matrix for dizygotic twins:

$$13. \begin{bmatrix} a^2 + c^2 + e^2 & \frac{1}{2}a^2 + c^2 \\ \frac{1}{2}a^2 + c^2 & a^2 + c^2 + e^2 \end{bmatrix}$$

The parameters in matrix (12) and (13), are estimated using a statistical software package that permit fitting of structural equation models, in our case this is Mx. Mx can use a raw data approach when fitting data to structural equation models. This is done by specifying starting values for each parameter. As described earlier Mx calculates a -2 times logarithmic likelihood which is a probability estimate reflecting the estimated parameter values.

RESULTS

Table 1 shows the phenotypic correlations. A histogram representation of subjective well-being Q1 and Q2 scores respectively can be seen in figure 4 and 5. Subjective well-being scores have a fairly good spread, and are not strongly skewed. Both Q1 and Q2 are being fairly in line with a normal distribution assumption. Phenotypic correlations are in the direction one could expect with Q1 and Q2 correlations being fairly high and a moderate negative correlation between Q1 and MDD and Q2 and MDD.

Table 1 – Phenotypic correlations, 95% confidence intervals in parentheses

Q1 – Q2	Q1 - MDD	Q2 – MDD
0.48 (0.46,0.51)	-0.23 (-0.30,-0.15)	-0.29 (-0.35,-0.23)

Figure 4.

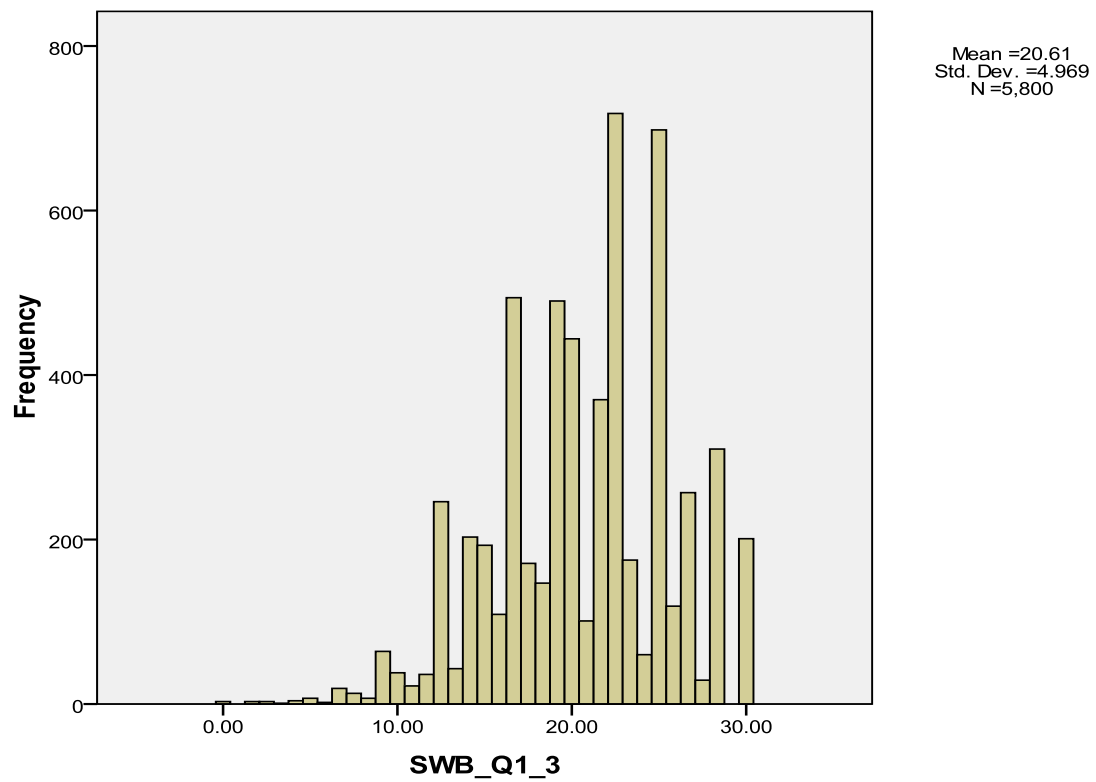


Figure 5.

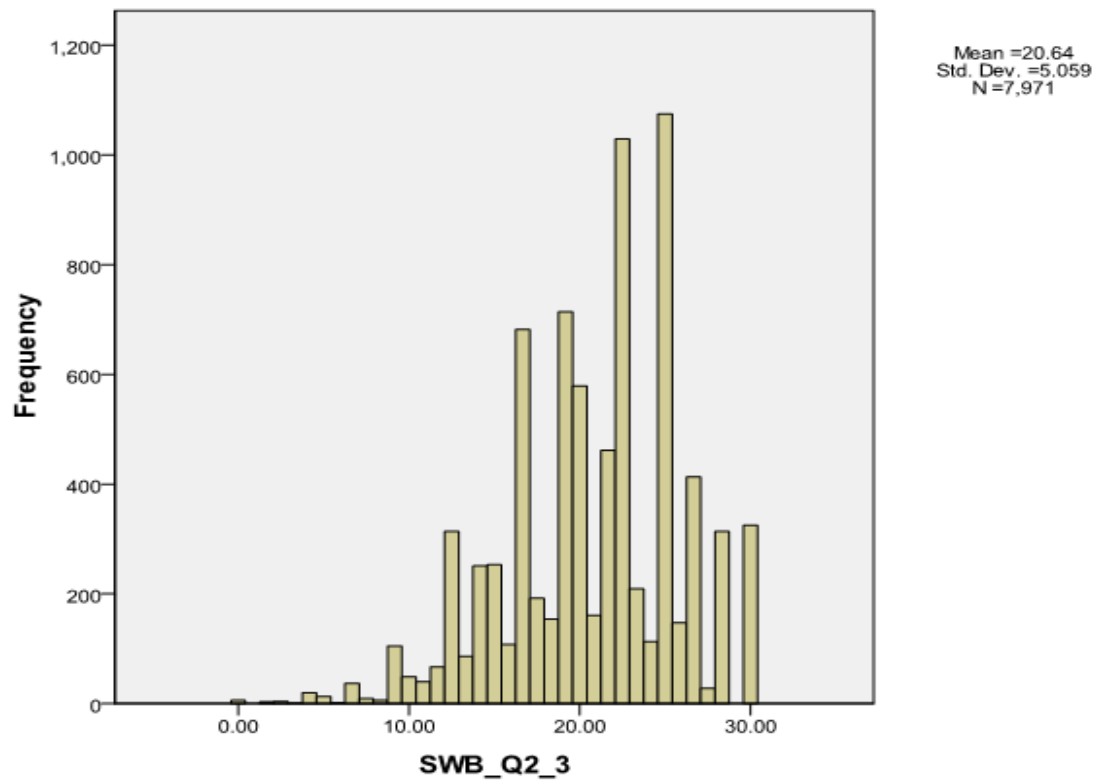


Table 2 – Polychoric correlations, 95% confidence intervals in parentheses

	Twin – Co – Twin correlations			Cross – trait cross – twin correlations		
	SWB Q1	SWB Q2	MDD	SWB Q1 – SWB Q2	SWB Q1 – MDD	SWB Q2 – MDD
Zygosity						
MZ	0.54 (0.49,0.56)	0.44 (0.39,0.48)	0.37 (0.21,0.52)	0.36 (0.32,0.41)	-0.27 (-0.38,-0.16)	-0.20 (-0.29,-0.11)
DZ	0.19 (0.14,0.24)	0.20 (0.16,0.24)	0.12 (0.00,0.29)	0.15 (0.11,0.19)	-0.10 (-0.20,-0.01)	-0.10 (-0.18,-0.01)

Table 2 shows both the twin-co-twin correlations and the cross-trait cross-twin correlations. Twin-co-twin correlations are the correlations between twin 1 and twin 2 on the same phenotype at the same time, whereas cross-trait cross-twin correlations meaning the correlations between twin 1 and twin 2 on different phenotypes. The twin-co-twin correlations and cross-trait cross-twin correlations are generally in accordance with what one would expect if additive genetic influence was present. If additive genetic influence is the main source of variation one would expect that the correlations in dizygotic pairs to be half as high as those in monozygotic pairs. Dominance deviations are expected if dizygotic correlations are $\frac{1}{4}$ of monozygotic correlations. In this correlation matrix, there are possibly the twin –co –twin correlations of SWB Q1 and MDD that might indicate dominance deviation. However due to the fact that twin modeling may lack power to detect dominance pattern (Neale, Eaves, and Kendler, 1994) and due to the scope of this paper, only an additive model was parameterized. The cross-trait cross-twin correlations also indicate an additive genetic model since the dizygotic correlations are close to half of what the monozygotic correlations are. Worth noting are the relatively wide confidence

intervals on the MDD correlations. However none of the confidence intervals except SWB Q2 – MDD are overlapping. Univariate analysis was carried out for four alternative models (ACE, AE, CE, E) on each of the three phenotypes. Results are shown in table 3. The ACE model where used as the saturated model which the sub-models are tested against. Mx does not yield and overall goodness of fit index for the full saturated model, the sub-models are chosen according to $\Delta\chi^2$ and ΔAIC . For all three phenotypes the best fitting model was an AE model, suggesting additive genetic influence and non-shared environmental influence to be the main sources of variation. This was in accordance with the analysis and predictions made from the correlation matrix.

Table 3

Univariate model fits for Major Depressive Disorder

Model	-2LL	$\Delta\chi^2$	Δdf	P	ΔAIC
ACE	2242.84				
AE	2242.84	0	1	Incalculable	-2.00
CE	2247.33	4.49	1	0.034	2.49
E	2264.15	21.32	2	0.00	17.32

Parameter estimation for major depressive disorder, 95% confidence intervals in parentheses

Model	a	c	e
Full	0.58 (0.18,0.69)	0 (0.00,0.49)	0.81 (0.72,0.90)
Best fitting (AE)	0.58 (0.44,0.69)	0	0.81 (0.72,0.90)

Univariate model fits for Subjective well-being Q1

Model	-2LL	$\Delta\chi^2$	Δdf	P	ΔAIC
ACE	20426.98				
AE	20426.98	0	1	Incalculable	-2.00
CE	20504.60	77.62	1	0	75.62
E	20729.84	302.86	2	0	298.86

Parameter estimation for subjective well-being Q1, 95% confidence intervals in parentheses

Model	a	c	e
Full	0.72 (0.68,0.75)	0 (0.00,0.19)	0.70 (0.66,0.73)
Best fitting (AE)	0.72 (0.68,0.75)	0	0.70 (0.66,0.73)

Univariate model fits for Subjective well-being Q2

Model	-2LL	$\Delta\chi^2$	Δdf	P	ΔAIC
ACE	28147.88				
AE	28147.88	0	1	Incalculable	-2.00
CE	281977.06	49.17	1	0	47.17
E	28453.55	305.69	2	0	301.67

Parameter estimation for subjective well-being Q2, 95% confidence intervals in parentheses

Model	a	c	e
Full	0.66 (0.63,0.69)	0 (0.00,0.27)	0.75 (0.72,0.78)
Best fitting (AE)	0.66 (0.63,0.69)	0	0.75 (0.72,0.78)

The univariate analysis yielded the background information necessary to carry on with the multivariate analysis. The results from the multivariate analysis are presented in figure 6. There are several important things to note here. First being that the association between additive genetic influence on subjective well-being and additive genetic influence on major depressive disorder is -0.58 this means that there is a substantially portion of the same genes that causes increase subjective well-being as well as major depressive disorder, but they work in opposite direction. Further there are an association between the non-shared environment which implies that different environmental stimulus causes major depressive disorder and subjective well-being. Further it is worth noting that additive genetic influence has a factor

loading of 0.88 on subjective well-being meaning that 77% of the variance in the latent subjective well-being measure can be explained by additive genetic influence, which is a substantial portion. The rest of the explained variance in subjective well-being is explained by non-shared environment which explains 23%. Further major depressive disorder is explained 33% by additive genetic influence and 65% by non-shared environmental influence.

Figure 6. 95% confidence intervals in parentheses

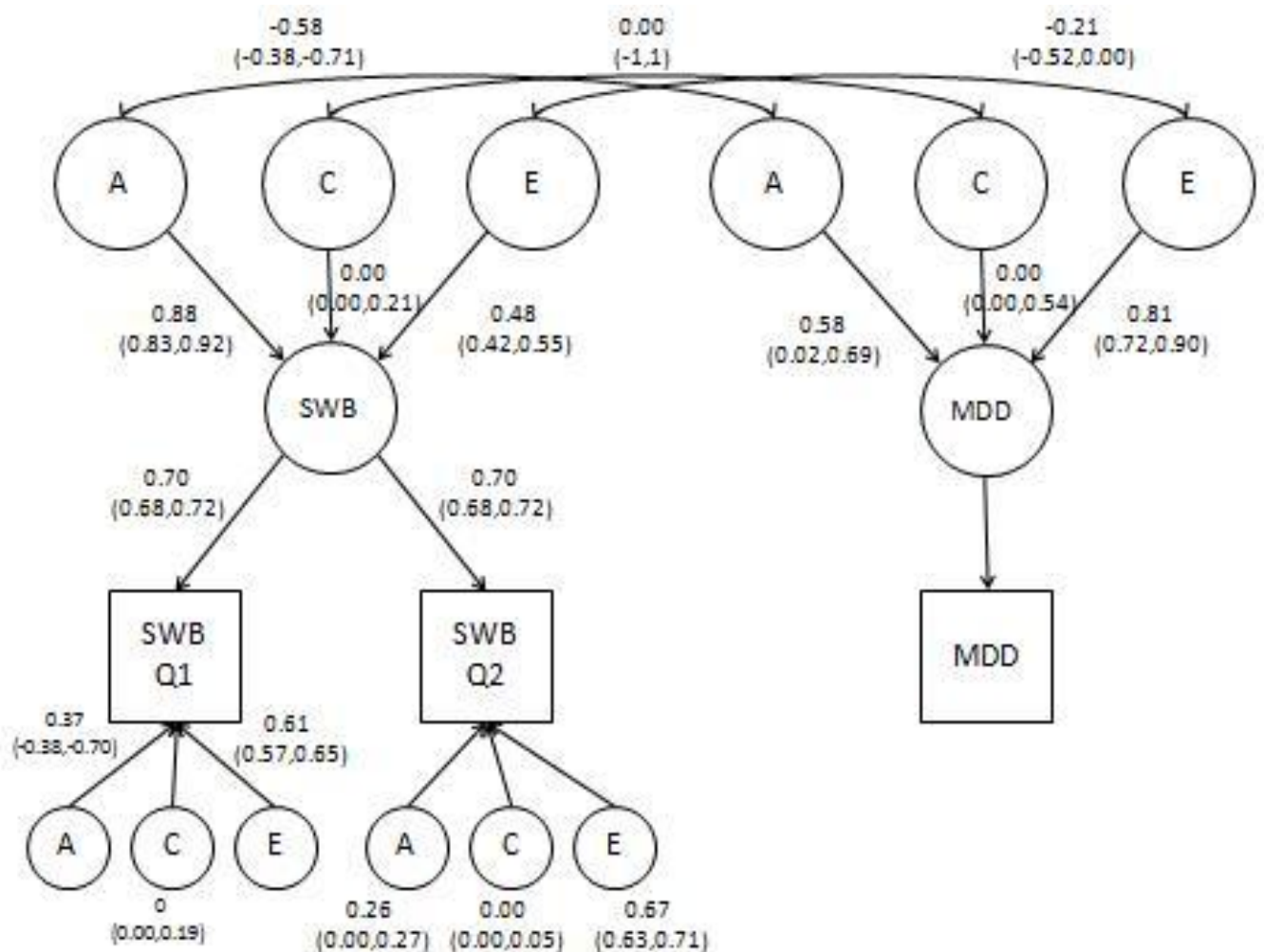


Figure 8 displays the saturated model, however several nested models were specified to analyze whether parameters could be dropped from the model without causing worse fit. As can be seen from table 4 additive genetic influence (A) cannot be dropped at any level in the model without resulting in a worse fit. However from these results shared environmental

influence (C) dropped from the entire model yielded the best fit (in bold). Considering the univariate results this is as expected.

Table 4.

Model	-2LL	$\Delta\chi^2$	Δdf	P	ΔAIC
Saturated model	49735.90				
Dropped specific A on Q1 and Q2	49750.68	14.78	2	0.001	10.78
Dropped specific C on Q1 and Q2	49735.90	0.00	2	Incalculable	-4.00
Dropped specific A and C on Q1 and Q2	49774.96	39.10	4	0.00	31.10
Dropped C from entire model	49735.90	0.00	5	Incalculable	-10.00
Dropped common A from latent SWB construct	49833.94	98.05	2	0.00	94.05
Dropped common A for SWB and MDD	49836.96	101.10	3	0.00	95.064

DISCUSSION

Before the discussion it could be of interest to recap what the research goals were. My first goal was to analyze the genetic and environmental contributions to subjective well-being and major depressive disorder. One aim was to investigate the genetic and environmental sources to each phenotype separately and to compare my findings to what previous research has found. The ultimate goal was to analyze to which degree these contributions were specific or common. That is, is subjective well-being caused by the same genes that cause major depressive disorder? To my knowledge, no study has previously looked at the specific or common contributions to the correlation between subjective well-being and major depressive disorder. These multivariate results will therefore be discussed in the sense that I will look at what these results will do for our understanding of the two phenotypes.

Univariate analysis

Heritability estimates for major depressive disorder in the univariate analysis was found to be 0.35. This is in accordance with what Sullivan et al. (2000) found in their meta-analysis of major depression. In their meta-analysis, Sullivan and colleagues (2000) estimated the heritability for major depression on the basis of six twin studies and reporting heritability in the range of 31%-42%. An AE model was found to be the best model to fit the data. Results from the present univariate analysis of major depressive disorder thus indicate that non-shared environmental influence plays a greater role in the etiology of major depressive disorder, than additive genetic influences, whereas shared environmental influences are negligible.

Heritability estimates for SWB based on the Q1 and Q2 data were estimated to be 0.52 and 0.44, respectively. The Q1 heritability results are somewhat on the high side compared to what Nes (2009) reported to be common heritability estimates for time specific subjective well-being estimates (35%-50%). However, not a great deal above taking into considerations confidence interval's ranging from 46% to 56%. The Q2 heritability estimates are in the range of what Nes (2009) reported. Best fitting model for both the Q1 and the Q2 assessments was an AE model. As previously pointed out (p. 3) this is in accordance with previous studies (e.g. Røysamb et al., 2002) whereas other studies have indicated contributions also from genetic dominance (Stubbe et al., 2005; Tellegen et al., 1988).

Worth noting for all three univariate analysis no shared environmental influences were found. This is in accordance with previous research (e.g. Nes et al., 2006; Stubbe et al., 2005). This was also expected from the correlation matrix presented in table 2. Shared environmental influence is assumed when dizygotic correlations are closer to monozygotic correlations than what one would expect out of additive genetic influence.

Multivariate analysis

The multivariate analysis uses a longitudinal approach for modeling subjective well-being. This enables us to look at the stable genetic and environmental component of subjective well-being. This is analogous to what Nes et al. (2006) has done although the specific model specification differed somewhat. The stable genetic component was estimated to account for 77% of the variation in the subjective well-being construct. The non-shared environment explained 23% of the variation. As mentioned earlier, the idea of using the two measurements as a basis for a latent subjective well-being construct enables us to abstract what is common between the two measurements and thus end up with a measure of stable , or

“trait-like” subjective well-being. Worth noting is that some time-specific additive genetic influence are indicated at both Q1 and Q2. A reasonable explanation for this might be that there different genes are of importance for subjective well-being at different stages in life. Another point worth noting is that the non-shared environmental influence on the latent subjective well-being construct might be an expression of a “purer” non-shared environmental influence. As the non-shared environment in twin modeling also comprises measurement error, the fact that we have used what is common for two measurements mean that the measurement error is left in the specific non-shared environment attached to Q1 and Q2. The major depressive disorder construct comprises of one measurement, thus it is reasonable to assume that the non-shared environment attached to the major depressive disorder construct comprises of more measurement error. If the reliability of the major depressive disorder construct had increased (i.e. by adding several measurements) this could have resulted in a greater correlation between the non-shared environment of major depressive disorder and subjective well-being construct, because of less measurement error. Nes et al. (2006) found that 80% of the stability in subjective well-being was attributable to additive genetic influence. Worth noting is that this finding used an overlapping sample with the present study, and that the subjective well-being scale used in the study by Nes et al. (2006) included one more item. This finding also mirrors the results from Lykken and Tellegen (1996) reviewed earlier, in which they found that genetic factors explained 80% of the stable variance in the Well-Being scale of the Multidimensional Personality Questionnaire.

Correlation between Major Depression and Subjective Well-Being

One of the most intriguing finding from this study is the correlation between additive genetic influence for major depressive disorder and subjective well-being. This correlation was estimated to -0.58 meaning that a substantial portion of the genes involved in subjective well-being also are involved in major depressive disorder. The minus implies that genes “work” in opposite direction. This finding will be discussed in the next section in relation to the covitality construct, if well-being and ill-being are spectrum or distinct constructs, and finally what implications findings reported here might have.

The substantial genetic basis for subjective well-being has been documented repeatedly and subjective well-being has been shown to have a genetic overlap with personality domains associated with elevated levels of subjective well-being such as extraversion (high), conscientiousness, and neuroticism (low) (Weiss et al., 2008). This has

led some researchers to suggest the presence of a partly genetic covitality factor (i.e. Weiss et al., 2002; Figueredo, Vásquez, Brumbach, and Schneider, 2007). A covitality factor may be contrasted with the findings of Kendler et al. (2003) who demonstrated that liability to internalizing disorders are attributable to shared genes. Likewise, covitality thought to reflect, at partly, genetic factor causing correlation between positive phenotypes. The results from this study, however, challenges the position to some degree that vitality and morbidity are distinct constructs at least from a genetic point of view. Because of the correlation observed between major depressive disorder and subjective well-being for additive genetic influences.

Ryff et al. (2006) used several biological markers known to be associated with several ill-being constructs such as depression, trait anger, and trait anxiety and with several well-being constructs such as positive/negative affect and personal growth. Their mission was to test whether ill-being and well-being are distinct constructs or spectrum constructs. Their rationale was that if a biomarker is associated with an ill-being construct but not with a well-being construct, this supports the distinct construct hypothesis (and vice-versa). If however, a biomarker is associated with a well-being construct and in opposite direction associated with an ill-being construct this supports the spectrum (mirror) hypothesis (Ryff et al., 2006). Seven biomarkers supported the distinct construct hypothesis, the most important for this discussion was the result that elevated levels of a biomarker called DHEA-S was associated with depressive symptoms, but not with any well-being constructs (supporting distinct construct hypothesis) (Ryff et al., 2006). A biomarker that supported the spectrum hypothesis and are of particular interest for this study is the result that individuals with high levels of negative affect (and trait anxiety and trait anger) had elevated levels of glycosylated hemoglobin, whereas individuals with higher levels of positive relations had lower levels of this biomarker, supporting a spectrum hypothesis (Ryff et al., 2006). The second biomarker that indicated a spectrum hypothesis was weight; individuals with higher weight reported more depressive symptoms, whereas individuals with lower weight reported more positive relations (Ryff et al., 2006). Worth noting was that the sample in this study comprised of women in the age range of 61 to 91 years old, and the total sample comprised of 135 individuals. If this can be generalized to a wider population remains to be further explored. Of particular interest for this study is the fact that the negative affect biomarker in the Ryff et al. (2006) study supports a spectrum or mirror hypothesis. However, depressive symptoms in the Ryff et al. (2006) study had a biomarker supporting the distinct hypothesis. The results of the Ryff et al. (2006) study and the circumplex model as proposed by Russel and Carroll (1999) supports the fact that at

least negative and positive affect may be best understood as two opposites of continuum. This may shed some light over the results from this study, as negative and positive affect is measured both in the subjective well-being scale and in the M-CIDI.

The greater question posed by studies such as this one along with the studies by Ryff et al. (2006), Larsen et al., (2001), and Russel and Carroll (1999), are: is well-being just the opposite of ill-being? Well-being as we have measured it can be said from a genetic point of view to be at least partly related to ill-being. In this study the correlation between major depressive disorder and subjective well-being was -0.58 and -0.21 for additive genetic influences and non-shared environmental influences respectively. The correlation between the two additive genetic components reflects that there is a great deal of genetic overlap between well-being and ill-being. Implications of this might be that relieving individuals of major depression symptoms can increase subjective well-being. Or to turn it around increasing subjective well-being as done by for instance well-being therapy (Fava, 1999) will relieve individuals of major depression symptoms.

STUDY LIMITATIONS

Cronbachs alpha for Q1 and Q2 were 0.64 and 0.67 respectively. This is somewhat in the lower region of what is regarded as acceptable. However the subjective well-being scale comprised of just three items, and the algorithm for computing the alpha rewards number of items, thus 0.64 and 0.67 was regarded as acceptable. The non-shared environmental component in twin modeling also incorporates measurement error, however. This will tend to, inflate the non-shared environmental influence and to deflate the genetic influence to.

Recruitment and attrition bias are possible threats to longitudinal research designs. Tambs, Rønning, Prescott, Kendler, Reichborn-Kjennerud, Torgersen, and Harris (2009) examined the NIPH Twin Panel for recruitment and attrition biases. Several factors predicted participation such as female sex, older age, higher education, monozygosity, high well-being and stomach/intestine illness (Tambs et al., 2009). A potential threat to the equal environment assumption, namely co-twin contact did not predict participation, however. In Q1 male single responders also reported more depression and anxiety symptoms on the SCL-5 than male pairwise responders (Tambs et al., 2009). Nes et al. (2006) reported on an overlapping sample with the one used here, that significant differences were observed

between continuers and drop-outs. This suggests that our conclusions may not be fully accurate reflections of the entire population.

Our results are also based on fairly young adult Norwegian twins and may thus not extrapolate to other age groups or nationalities,

Lastly our measurements especially for subjective well-being are crude and results should be considered with caution.

CONCLUSION

In summary, stable subjective well-being was found to be highly heritable and best explained by a model including additive genetic effects and non-shared environmental effects. Major depressive disorder had somewhat lower heritability, but was also best explained by a model comprising of additive genetic effects and non-shared environmental influences. Major depressive disorder and subjective well-being were found to have a substantial overlap in genetic basis and a smaller overlap in non-shared environmental influence.

REFERENCES

- American Psychiatric Association (2000). *Diagnostic and Statistical Manual of Mental Disorders* (4th ed.). Text Revision. Washington, DC: Author
- Baker, L. A. (2007). Foundation of Behavioral Genetics: Student Recipients of the Thompson Award. *Behavioral Genetics*, 37, 727-733. doi: 10.1007/s10519-007-9181-0
- Beckwith, J. (2006). Whither Human Behavioral Genetics? In E. Parens, A. R. Chapman, and N. Press (Eds.), *Wrestling with Behavioral Genetics* (pp. 74-99). Baltimore: The John Hopkins University Press
- Bell, R. Q. (1968). A Reinterpretation of the Direction of Effects in Studies of Socialization. *Psychological Review*, 75, 81-95. doi: 10.1037/h0025583
- Bollen, K. A. (1989). *Structural Equations with Latent Variables*. New York: John Wiley & Sons, Inc
- Caspi, A., Sugden, K., Moffitt, T. E., Taylor, A., Craig, I. W., Harrington, H., McClay, J., ... Poulton, R. (2003). Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene, *Science*, 301, 386-389. doi:10.1126/science.1083968
- Costa, P. T., and McCrae, R. R. (1980). Influence of Extraversion and Neuroticism on Subjective Well-Being: Happy and Unhappy People. *Journal of Personality and Social Psychology*, 38 (4), 668-678. doi: 10.1037/0022-3514.38.4.668
- Cloninger, C. R., Svrakic, D. M., and Przybeck, T. R. (2006). Can personality assessment predict future depression? A twelve-month follow-up of 631 subjects. *Journal of Affective Disorders*, 92, 35-44. doi: 10.1016/j.jad.2005.12.034
- DeNeve, K. M., and Cooper, H. (1998). The Happy Personality: A Meta-Analysis of 137 Personality Traits and Subjective Well-Being. *Psychological Bulletin*. 124 (2), 197-229. doi: 10.1037/0033-2909.124.2.197
- Diener, E., Lucas, R. E., and Oishi, S. (2005). Subjective Well-Being. The Science of Happiness and Life Satisfaction. In C. R. Snyder and S. J. Lopez (Eds.), *Handbook of Positive Psychology* (pp. 63-73). New York: Oxford University Press

- Diener, E., Sandvik, E., Seidlitz, L., and Diener, M. (1993). The Relationship Between Income and Subjective Well-Being: Relative or Absolute? *Social Indicators Research*, 28, 195-223. doi:10.1007/BF01079018
- Diener, E., Scollon, C. N., and Lucas, R. E. (2003). The evolving concept of subjective well-being: the multifaceted nature of happiness. *Advances in Cell Aging and Gerontology*, 15, 187-219. doi: 10.1016/S1566-3124(03)15007-9
- Dominicus, A., Skrondal, A., Gjessing, H. K., Pedersen, N. L., and Palmgren, J. (2006). Likelihood Ratio Tests in Behavioral Genetics: Problems and Solutions. *Behavior Genetics*, 36 (2), 331-340. doi: 10.1007/s10519-005-9034-7
- Fava, G. A. (1999). Well-Being Therapy: Conceptual and Technical Issues. *Psychotherapy and Psychosomatics*, 68, 171-179. doi: 10.1159/000012329
- Figueredo, A. J., Vásquez, G., Brumbach, B. H., and Schneider, S. M. R. (2007). The K-Factor, Covitality, and Personality. A Psychometric test of Life History Theory. *Human Nature*, 18 (1), 47-73. doi: 10.1007/BF02820846
- Gillespie, N. A., Whitfield, J. B., Williams, B., Heath, A. C., and Martin, N. G. (2005). The relationship between stressful life events, the serotonin transporter (5-HTTLPR) genotype and major depression. *Psychological Medicine*, 35, 101-111. doi:10.1017/S0033291704002727
- Hansson, A., Forsell, Y., Hochwälder, J., and Hillerås, P. (2008). Impact of changes in life circumstances on subjective well-being in an adult population over a 3-year period. *Public Health*, 122, 1392-1398. doi:10.1016/j.puhe.2008.05.020
- Harris, J. R., Magnus, P., and Tambs, K. (2002). The Norwegian Institute of Public Health Twin Panel: A Description of the Sample and Program of Research. *Twin Research*, 5 (5), 415-423
- Johnson, W., Krueger, R. F., Bouchard, T. J., and McGue, M. (2002). The Personalities of Twins: Just Ordinary Folks. *Twin Research*, 5 (2), 125-131.
- Joseph, J. (2004). *The Gene Illusion. Genetic Research in Psychiatry and Psychology Under the Microscope*. New York: Algora Publishing.

- Khoury, M. J., Beaty, T. H., and Cohen, B. H. (1993). *Fundamentals of Genetic Epidemiology*. New York: Oxford University Press.
- Kendler, K. S. (2005). Psychiatric Genetics: A Methodologic Critique. *American Journal of Psychiatry*, 162, 3-11.
- Kendler, K. S., and Gardner, C. O. (1998). Twin studies of adult psychiatric and substance dependence disorders: are they biased by differences in the environmental experiences of monozygotic and dizygotic twins in childhood and adolescence? *Psychological Medicine*, 28, 625-633. doi: 10.1017/S0033291798006643
- Kendler, K. S., Gatz, M., Gardner, C. O., and Pedersen, N. L. (2006). Personality and Major Depression. A Swedish Longitudinal, Population-Based Twin Study. *Archives of General Psychiatry*, 63, 1113-1120.
- Kendler, K. S., Kessler, R. C., Walters, E. E., MacLean, C., Neale, M. C., Heath, A. C., Phil, D., and Eaves, L. J. (1995). Stressful Life Events, Genetic Liability, and Onset of an Episode of Major Depression in Women. *American Journal of Psychiatry*, 152 (6), 833-842
- Kendler, K. S., Kuhn, J. W., Vittum, J., Prescott, C. A., and Riley, B. (2005). The Interaction of Stressful Life Events and a Serotonin Transporter Polymorphism in the Prediction of Episodes of Major Depression. A Replication. *Archives of General Psychiatry*, 62, 529-535.
- Kendler, K. S., and Prescott, C. A. (2006). *Genes, Environment, and Psychopathology. Understanding the Causes of Psychiatric and Substance Use Disorders*. New York: The Guilford Press
- Kendler, K. S., Prescott, C. A., Myers, J., and Neale, M. C. (2003). The Structure of Genetic and Environmental Risk Factors for Common Psychiatric and Substance Use Disorders in Men and Women. *Archives of General Psychiatry*, 60, 929-937.
- Kessler, R. C., Berglund, P., Demler, O., Jin, R., Koretz, D., Merikangas, K. R., Wang, P. S. (2003). The Epidemiology of Major Depressive Disorder. Results From the National Comorbidity Survey Replication (NCS-R). *Journal of American Medical Association*, 289, 3095-3105. doi:10.1001/jama.289.23.3095

- Kringle, E., Torgersen, S., and Cramer, V. (2001). A Norwegian Psychiatric Epidemiological Study. *American Journal of Psychiatry*, 158, 1091-1098.
- Krueger, R. F., and Markon, K. E. (2006). Reinterpreting Comorbidity: A Model-Based Approach to Understanding and Classifying Psychopathology. *Annual Review of Clinical Psychology*, 2, 111-133. doi: 10.1146/annurev.clinpsy.2.022305.095213
- Loehlin, J. C., and Nichols, R. C. (1976). *Heredity, environment, and personality*. Austin: University of Texas Press
- Lorant, V., Delière, D., Eaton, W., Robert, A., Philippot, P., and Ansseau, M. (2003). Socioeconomic Inequalities in Depression: A Meta-Analysis. *American Journal of Epidemiology*, 157, 98-112. doi: 10.1093/aje/kwf182
- Larsen, J. T., McGraw, A. P., and Cacioppo, J. T. (2001). Can People Feel Happy and Sad at the Same Time? *Journal of Personality and Social Psychology*, 81 (4), 684-696. doi: 10.1037//0022-3514.81.4.684
- Lykken, D., and Tellegen, A. (1996). Happiness Is a Stochastic Phenomenon. *Psychological Science*, 7 (3), 186-189.
- Mineka, S., Watson, D., and Clark, L. A. (1998). Comorbidity of Anxiety and Unipolar Mood Disorders. *Annual Review of Psychology*, 49, 377-412. doi: 10.1146/annurev.psych.49.1.377
- Morrison, M. (2002). Modelling Populations: Pearson and Fisher on Mendelism and Biometry. *British Journal for the Philosophy of Science*, 53, 39-68. doi:10.1093/bjps/53.1.39
- Mykletun, A., Knudsen, A. K., and Schjelderup Mathiesen, K. (2009). *Psykkiske lidelser i Norge: Et folkehelseperspektiv*. Nydalen: Nordberg Trykk AS.
- Neale, M. C., Eaves, L. J., and Kendler, K. S. (1994). The Power of the Classical Twin Study to Resolve Variation in Threshold Traits. *Behavior Genetics*, 24 (3), 239-258. doi: 10.1007/BF01067191
- Neale, M. C., and Maes, H. H. M. (2000). *Methodology for Genetic Studies of Twins and Families*. Dordrecht: Kluwer Academic Publishers B.V.

- Nes, R. B. (2009). Happiness in Behaviour Genetics: Findings and Implications. *Journal of Happiness Studies*. Advance online publication. doi:10.1007/s10902-009-9145-6
- Nes, R. B., Røysamb, E., Tambs, K., Harris, J. R., and Reichborn-Kjennerud, T. (2006). Subjective well-being: genetic and environmental contributions to stability and change. *Psychological Medicine*, 36, 1033-1042. doi:10.1017/S0033291706007409.
- Pavot, W., and Diener, E. (1993). Review of the Satisfaction With Life Scale. *Psychological Assessment*, 5 (2), 164-172. doi: 10.1037/1040-3590.5.2.164
- Plomin, R., DeFries, J. C., McClearn, G. E., and McGuffin, P. (2008). *Behavioral Genetics* (5th ed.). New York: Worth Publishers.
- Purcell, S. (2008). Statistical Methods in Behavioral Genetics. In R. Plomin, J. C. DeFries, G. E. McClearn, and P. McGuffin. *Behavioral Genetics* (5th ed). (pp. 359-410). New York: Worth Publishers.
- Russel, J. A., and Carroll, J. M. (1999). On the Bipolarity of Positive and Negative Affect. *Psychological Bulletin*, 125 (1), 3-30. doi: 10.1037/0033-2909.125.1.3
- Rutter, M., Moffitt, T. E., and Caspi, A. (2006). Gene-Environment interplay and psychopathology: multiple varieties but real effects. *Journal of Child Psychology and Psychiatry*, 47, 226-261. doi:10.1111/j.1469-7610.2005.01557.x
- Ryff, C. D., Love, G. D., Urry, H. L., Muller, D., Rosenkranz, M. A., Friedman, E. M., Davidson, R. J., and Singer, B. (2006). Psychological Well-Being and Ill-Being: Do They Have Distinct or Mirrored Biological Correlates? *Psychotherapy and Psychosomatics*. 75, 85-95. doi: 10.1159/000090892
- Røysamb, E., Harris, J. R., Magnus, P., Vittersø, J., and Tambs, K. (2002). Subjective well-being. Sex-specific effects of genetic and environmental factors. *Personality and Individual Differences*, 32, 211-223. doi:10.1016/S0191-8869(01)00019-8
- Røysamb, E., Tambs, K., Reichborn-Kjennerud, T., Neale, M. C., and Harris, J. R. (2003). Happiness and Health: Environmental and Genetic Contributions to the Relationship Between Subjective Well-Being, Perceived Health, and Somatic Illness. *Journal of Personality and Social Psychology*, 85 (6), 1136-1146. doi:10.1037/0022-3514.85.6.1136

- Schultz, D. P., and Schultz, S. E. (1996). *A History of Modern Psychology* (6th ed.). Orlando: Harcourt Brace & Company.
- Seligman, M. E. P., and Csikszentmihalyi, M. (2000). Positive Psychology. An Introduction. *American Psychologist*, 55, 5-14. doi: 10.1037//0003-066X.55.1.5
- Seligman, M. E. P., Walker, E. F., and Rosenhan, D. L. (2001). *Abnormal Psychology* (4th ed.). New York: W. W. Norton & Company, Inc.
- Stubbe, J. H., Posthuma, D., Boomsma, D. I., and DeGeus, E. J. C. (2005). Heritability of life satisfaction in adults: a twin-family study. *Psychological Medicine*, 35, 1581-1588. doi:10.1017/S0033291705005374
- Suh, E., Diener, E., and Fujita, F. (1996). Events and Subjective Well-Being: Only Recent Events Matter. *Journal of Personality and Social Psychology*, 70 (5), 1091-1102. doi: 10.1037/0022-3514.70.5.1091
- Sullivan, P. F., Neale, M. C., and Kendler, K. S. (2000). Genetic Epidemiology of Major Depression: Review and Meta-Analysis. *American Journal of Psychiatry*, 157, 1552-1562.
- Tambs, K., Rønning, T., Prescott, C. A., Kendler, K. S., Reichborn-Kjennerud, T., Torgersen, S., and Harris, J. R. (2009). The Norwegian Institute of Public Health Twin Study of Mental Health: Examining Recruitment and Attrition Bias. *Twin Research and Human Genetics*, 12 (2) 158-168.
- Tellegen, A., Lykken, D. T., Bouchard, T. J., Wilcox, K. J., Segal, N. L., and Rich, S. (1988). Personality Similarity in Twins Reared Apart and Together. *Journal of Personality and Social Psychology*, 54 (6), 1031-1039. doi: 10.1037/0022-3514.54.6.1031
- Turkheimer, E., and Waldron, M. (2000). Nonshared Environment: A Theoretical, Methodological, and Quantitative Review. *Psychological Bulletin*, 126, 78-108. doi: 10.1037/0033-2909.126.1.78
- Watson, D., and Kendall, P. C. (1989). Understanding Anxiety and Depression: Their Relation to Negative and Positive Affective States. In P. C. Watson and D. Watson (Eds.), *Anxiety and Depression. Distinctive and Overlapping Features* (pp. 3-26). San Diego: Academic Press, Inc.

- Weiss, A., Bates, T. C., and Luciano, M. (2008). Happiness Is a Personal(ity) Thing. The Genetics of Personality and Well-Being in a Representative Sample. *Psychological Science*, 19 (3), 205-210. doi: 10.1111/j.1467-9280.2008.02068.x
- Weiss, A., King, J. E., and Enns, R. M. (2002). Subjective Well-Being Is Heritable and Genetically Correlated With Dominance in Chimpanzees (*Pan troglodytes*). *Journal of Personality and Social Psychology*, 83 (5), 1141-1149. doi:10.1037//0022-3514.83.5.1141
- Wilson, W. (1967). Correlates of Avowed Happiness. *Psychological Bulletin*, 67 (4), 294-306. doi: 10.1037/h0024431
- Wittchen, H. -U., Lachner, G., Wunderlich, U., and Pfister, H. (1998). Test-retest reliability of the computerized DSM-IV version of the Munich-Composite International Diagnostic Interview (M-CIDI). *Social Psychiatry and Psychiatric Epidemiology*, 33, 568-578. doi: 10.1007/s001270050095